

SEQUENCE LISTING

<110> Sticklen, Masomeh B
 Maqbool, Shahina B
 Dale, Bruce E

<120> TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
 DEGRADE
 LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS

<130> MSU 4.1-539

<150> 60/242,408

<151> 2000-10-20

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 1110

<212> DNA

<213> Oryza sativa

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Leu Gly Tyr Asn Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys
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Pro Gly Thr Met Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp
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Ala Gly Gln Ile Gly Leu Arg Ile Ile Leu Asp Arg His Arg Pro Asp
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Cys Ser Gly Gln Ser Ala Leu Trp Tyr Thr Ser Ser Val Ser Glu Ala
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Arg Ala Gly Asn Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe
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Val Glu Gly Val Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly
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Arg Leu Val Tyr Ser Ala His Asp Tyr Ala Thr Ser Val Tyr Pro Gln
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Asn Lys Asn Trp Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp
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Met	Asn	Asp	His	Leu	Val	Gln	Val	Ala	Glu	Ala	Ile	Ala	Asp	Gly	Val		
			405					410						415			
gag	gtc	ctg	ggc	tac	acc	tcc	tgg	ggc	tgc	atc	gac	ctg	gtc	tcg	gcc	1296	
Glu	Val	Leu	Gly	Tyr	Thr	Ser	Trp	Gly	Cys	Ile	Asp	Leu	Val	Ser	Ala		
		420						425					430				
tcc	acc	gcc	cag	atg	tcc	aag	cgc	tac	ggg	ttc	atc	tac	gtg	gac	cgt	1344	
Ser	Thr	Ala	Gln	Met	Ser	Lys	Arg	Tyr	Gly	Phe	Ile	Tyr	Val	Asp	Arg		
		435				440					445						
gac	gac	ggc	ggc	aac	ggc	acc	ctg	gcc	cgc	tac	cgc	aag	aag	tcc	ttc	1392	
Asp	Asp	Gly	Gly	Asn	Gly	Thr	Leu	Ala	Arg	Tyr	Arg	Lys	Lys	Ser	Phe		
	450					455					460						
ggc	tgg	tac	cgc	gac	gtc	atc	gcc	tcc	aac	ggg	gcc	tcc	ctc	gtg	cct	1440	
Gly	Trp	Tyr	Arg	Asp	Val	Ile	Ala	Ser	Asn	Gly	Ala	Ser	Leu	Val	Pro		
465					470				475						480		
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Pro	Val	Gln	Glu	Pro	Pro	Arg	Gly										
				485													

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 <211> 488
 <212> PRT
 <213> Actinomyces naeslundii

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 <222> (113)..(113)
 <223> The 'Xaa' at location 113 stands for Leu.

 <220>
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 <222> (148)..(148)
 <223> The 'Xaa' at location 148 stands for Asp, Gly, Ala, or Val.

 <220>
 <221> misc_feature
 <222> (316)..(316)
 <223> The 'Xaa' at location 316 stands for Tyr, Cys, Ser, or Phe.

 <220>
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 <222> (339)..(339)
 <223> nucleotide is uncertain

 <220>
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Tyr	Asn	Glu	Asp	Gly	Lys	Gly	Leu	Ser	Val	Gln	Asp	Val	Met	Pro	Arg	35	40	45	
Gly	Ile	Met	Ala	His	Pro	Thr	Gln	Ala	Pro	Thr	Pro	Asp	Asn	Leu	Gln	50	55	60	
Ala	Arg	Gly	Asp	Arg	Pro	Ser	Thr	Thr	Ala	Tyr	Ala	Glu	Asp	Ile	Ser	65	70	75	80
Leu	Phe	Ala	Glu	Met	Gly	Phe	Lys	Val	Phe	Arg	Phe	Ser	Ile	Ala	Trp	85	90	95	
Ser	Arg	Ile	Phe	Pro	Leu	Gly	Asp	Glu	Thr	Glu	Pro	Asn	Glu	Glu	Gly	100	105	110	
Xaa	Ala	Phe	Tyr	Asp	Arg	Val	Leu	Asp	Glu	Leu	Glu	Lys	His	Gly	Ile	115	120	125	
Glu	Pro	Leu	Val	Thr	Ile	Ser	His	Tyr	Glu	Thr	Pro	Leu	His	Leu	Ala	130	135	140	
Arg	Thr	Tyr	Xaa	Gly	Trp	Thr	Asp	Arg	Arg	Leu	Ile	Gly	Phe	Phe	Glu	145	150	155	160
Arg	Tyr	Ala	Arg	Thr	Leu	Phe	Glu	Arg	Tyr	Gly	Lys	Arg	Val	Lys	Tyr	165	170	175	
Trp	Leu	Thr	Phe	Asn	Glu	Ile	Asn	Ser	Val	Leu	His	Glu	Pro	Phe	Leu	180	185	190	
Ser	Gly	Gly	Val	Ala	Thr	Pro	Lys	Asp	Arg	Pro	Pro	Glu	Gln	Asp	Leu	195	200	205	
Tyr	Gln	Ala	Ile	Gln	Asn	Glu	Leu	Val	Ala	Ser	Ala	Ala	Ala	Thr	Arg	210	215	220	
Ile	Ala	His	Glu	Thr	Asn	Pro	Asp	Ile	Gln	Val	Gly	Cys	Met	Ile	Leu	225	230	235	240

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260 265 270

Arg Gly Glu Tyr Pro Gly Tyr Leu Arg Arg Thr Leu Arg Asp Lys Gly
275 280 285

Ile Glu Leu Glu Ile Thr Glu Glu Asp Arg Val Leu Leu Arg Glu His
290 295 300

Thr Val Asp Phe Val Ser Phe Ser Tyr Tyr Met Xaa Val Cys Glu Thr
305 310 315 320

Val Thr Gln Ser Ala Glu Ala Gly Arg Gly Asn Leu Met Gly Gly Val
325 330 335

Pro Asn Pro Thr Leu Glu Ala Ser Glu Trp Gly Trp Gln Ile Asp Pro
340 345 350

Ala Gly Leu Arg Thr Ile Leu Asn Asp Tyr Trp Asp Arg Trp Gly Lys
355 360 365

Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val Leu Val
370 375 380

Asp Gly Pro Asn Gly Pro Thr Val Glu Asp Asp Tyr Arg Ile Ala Tyr
385 390 395 400

Met Asn Asp His Leu Val Gln Val Ala Glu Ala Ile Ala Asp Gly Val
405 410 415

Glu Val Leu Gly Tyr Thr Ser Trp Gly Cys Ile Asp Leu Val Ser Ala
420 425 430

Ser Thr Ala Gln Met Ser Lys Arg Tyr Gly Phe Ile Tyr Val Asp Arg
435 440 445

Asp Asp Gly Gly Asn Gly Thr Leu Ala Arg Tyr Arg Lys Lys Ser Phe
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Pro Val Gln Glu Pro Pro Arg Gly
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 <223> 1,6-alpha-glucanhydrolase

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aagtgctagc tcagaaacgc ttgtagccag tgaagcacta gtcctgaggt cagctgctgt	180
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tccagaaaca acaaaagcag cttatagcaa gacagatggt gatattaatt attcogttgt	360
tgtgtctaat ccaacagcag aaactaagac g atg act gtc aac ttg aca ctt	412
Met Thr Val Asn Leu Thr Leu	
1 5	
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Gln His Ala Ser Glu Ile Ile Gly Gln Asp Asn Val Asp Leu Thr Leu	
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Ala Ala Gly Ala Ser Ala Lys Val Ser Asn Leu Thr Val Ala Ser Glu	
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tgg ttg aca aac aat aca ggt tac ttg gtg aca atc agt gtc aac gat	556
Trp Leu Thr Asn Asn Thr Gly Tyr Leu Val Thr Ile Ser Val Asn Asp	
40 45 50 55	
aaa tca ggc aat gtc ttg tca agc aag cgc gct ggc ttg tct gtt gaa	604
Lys Ser Gly Asn Val Leu Ser Ser Lys Arg Ala Gly Leu Ser Val Glu	
60 65 70	
gat gat tgg aca gtt ttc cca cgt tac ggt atc gta gca ggt tca cca	652
Asp Asp Trp Thr Val Phe Pro Arg Tyr Gly Ile Val Ala Gly Ser Pro	
75 80 85	
act gat caa aac agt att ctt gtt aaa aat ctt gaa gcc tac cgt aaa	700
Thr Asp Gln Asn Ser Ile Leu Val Lys Asn Leu Glu Ala Tyr Arg Lys	
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gag ctt gag ctc atg aag tct atg aat atc aac tca tat ttc ttc tat	748
Glu Leu Glu Leu Met Lys Ser Met Asn Ile Asn Ser Tyr Phe Phe Tyr	
105 110 115	
gat gct tat aat gaa gct aca gat cct ttc cca gaa ggt gtc gat agc	796
Asp Ala Tyr Asn Glu Ala Thr Asp Pro Phe Pro Glu Gly Val Asp Ser	
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ttt gtt caa aaa tgg aat acc tgg agt cac act cag gtt gac act aag	844
Phe Val Gln Lys Trp Asn Thr Trp Ser His Thr Gln Val Asp Thr Lys	
140 145 150	

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atg Met	ctt Leu	tat Tyr 170	aac Asn	atg Met	att Ile	tca Ser	gca Ala 175	gat Asp	tca Ser	aat Asn	cca Pro	aag Lys 180	aat Asn	ccg Pro	gcc Ala	940
ctt Leu	cca Pro 185	ctt Leu	gct Ala	gct Ala	ttg Leu	gct Ala 190	tat Tyr	aac Asn	ttc Phe	tac Tyr	gat Asp 195	agc Ser	ttt Phe	ggt Gly	aag Lys	988
aag Lys 200	ggg Gly	gaa Glu	ccg Pro	atg Met	act Thr 205	tac Tyr	act Thr	atc Ile	ggg Gly	gat Asp 210	aac Asn	cca Pro	act Thr	caa Gln	ggt Val 215	1036
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ggt Val	ggt Val	tat Tyr	aat Asn 315	gag Glu	ctt Leu	tgg Trp	aca Thr	aac Asn 320	ggg Gly	ggg Gly	tca Ser	ggt Val	att Ile 325	cca Pro	gga Gly	1372
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cgc Arg	aat Asn 345	aaa Lys	act Thr	ggg Gly	aaa Lys	tca Ser 350	ctt Leu	atc Ile	ggt Val	ggg Gly	gcc Ala 355	tac Tyr	atg Met	gaa Glu	gaa Glu	1468
cca Pro 360	ggg Gly	att Ile	gat Asp	tat Tyr	act Thr 365	ggt Val	cct Pro	ggc Gly	gga Gly	aaa Lys 370	gca Ala	act Thr	aac Asn	ggg Gly	gct Ala 375	1516
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Ala Ala Leu Ala Asn Ala Asn Ala Ala Leu Asn Val Leu Gln Ser Ala	
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Tyr Tyr Pro Thr Gln Tyr Leu Ser Val Ala Lys Asp Thr Ile Arg Lys	
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ctt tac aat tac caa cag ttt atc act gct tat gaa aat ctt ctc cgc	1756
Leu Tyr Asn Tyr Gln Gln Phe Ile Thr Ala Tyr Glu Asn Leu Leu Arg	
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Gly Glu Gly Val Thr Asn Ser Thr Gln Ala Val Ser Thr Lys Asn Ala	
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Ser Gly Glu Ile Leu Ser Lys Asp Ala Leu Gly Val Thr Gly Asp Gln	
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Val Trp Thr Phe Ala Lys Ser Gly Lys Gly Phe Ser Thr Val Gln Met	
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Ile Asn Met Met Gly Ile Asn Ala Gly Trp His Asn Glu Glu Gly Tyr	
505 510 515	
gcg gac aat aaa aca ccg gac gca caa gaa aat ctc aca gtt cgt ctt	1996
Ala Asp Asn Lys Thr Pro Asp Ala Gln Glu Asn Leu Thr Val Arg Leu	
520 525 530 535	
agc cta gca ggt aaa aca gcc caa gaa gca gct aaa att gct gat caa	2044
Ser Leu Ala Gly Lys Thr Ala Gln Glu Ala Ala Lys Ile Ala Asp Gln	
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Val Tyr Val Thr Ser Pro Asp Asp Trp Ala Thr Ser Ser Met Lys Lys	
555 560 565	
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Ala Gln Ala Ser Leu Glu Thr Asp Glu Asn Gly Gln Pro Val Leu Val	
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Ile Ser Val Pro Lys Leu Thr Leu Trp Asn Met Leu Tyr Ile Lys Glu	
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Asp Thr Thr Ala Thr Pro Val Glu Pro Val Thr Asn Gln Ala Gly Lys	
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Lys Val Asp Asn Thr Val Thr Ser Glu Ala Ser Ser Glu Thr Ala Lys	
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Ser Glu Asn Thr Thr Val Asn Lys Gly Ser Glu Ala Pro Thr Asp Thr	
635 640 645	
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Lys Pro Ser Val Glu Ala Pro Lys Leu Asp Glu Thr Thr Lys Pro Ala	
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cca tca gtt gac gag tta gta aac tca gca gct gtt cca gtg gcg ata	2428
Pro Ser Val Asp Glu Leu Val Asn Ser Ala Ala Val Pro Val Ala Ile	
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gct gtg tca gag acc gca cat gat aag aaa gat gac aac tca gta tct	2476
Ala Val Ser Glu Thr Ala His Asp Lys Lys Asp Asp Asn Ser Val Ser	
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715 720 725	
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Ser Gln Ala Ser Thr Ser Leu Val Ser Glu Thr Thr Ser Thr Ile Val	
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795 800 805	
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Leu Met Asp Tyr Gln Lys Thr Ser Ile Val Gly Ile Asp Ser Leu	
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 35 40 45
 Val Thr Ile Ser Val Asn Asp Lys Ser Gly Asn Val Leu Ser Ser Lys
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 Arg Ala Gly Leu Ser Val Glu Asp Asp Trp Thr Val Phe Pro Arg Tyr
 65 70 75 80
 Gly Ile Val Ala Gly Ser Pro Thr Asp Gln Asn Ser Ile Leu Val Lys
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 Asn Leu Glu Ala Tyr Arg Lys Glu Leu Glu Leu Met Lys Ser Met Asn
 100 105 110
 Ile Asn Ser Tyr Phe Phe Tyr Asp Ala Tyr Asn Glu Ala Thr Asp Pro
 115 120 125
 Phe Pro Glu Gly Val Asp Ser Phe Val Gln Lys Trp Asn Thr Trp Ser
 130 135 140
 His Thr Gln Val Asp Thr Lys Ala Val Lys Glu Leu Val Asp Gln Val
 145 150 155 160
 His Lys Ser Gly Ala Val Ala Met Leu Tyr Asn Met Ile Ser Ala Asp
 165 170 175
 Ser Asn Pro Lys Asn Pro Ala Leu Pro Leu Ala Ala Leu Ala Tyr Asn
 180 185 190
 Phe Tyr Asp Ser Phe Gly Lys Lys Gly Glu Pro Met Thr Tyr Thr Ile
 195 200 205
 Gly Asp Asn Pro Thr Gln Val Tyr Tyr Asp Pro Ala Asn Pro Asp Trp
 210 215 220
 Gln Lys Tyr Ile Ala Gly Val Met Lys Ser Ala Met Asp Arg Met Gly
 225 230 235 240
 Phe Asp Gly Trp Gln Gly Asp Thr Ile Gly Asp Asn Arg Val Thr Asp
 245 250 255
 Tyr Glu His Arg Asn Ser Thr Asp Glu Ala Asp Ser His Met Met Ser
 260 265 270
 Asp Ser Tyr Ala Ser Phe Ile Asn Ala Met Lys Asp Leu Ile Gly Glu
 275 280 285

Lys Tyr Tyr Ile Thr Ile Asn Asp Val Asn Gly Gly Asn Asp Asp Lys
290 295 300

Leu Ala Lys Ala Arg Gln Asp Val Val Tyr Asn Glu Leu Trp Thr Asn
305 310 315 320

Gly Gly Ser Val Ile Pro Gly Arg Met Gln Val Ala Tyr Gly Asp Leu
325 330 335

Lys Ala Arg Ile Asp Met Val Arg Asn Lys Thr Gly Lys Ser Leu Ile
340 345 350

Val Gly Ala Tyr Met Glu Glu Pro Gly Ile Asp Tyr Thr Val Pro Gly
355 360 365

Gly Lys Ala Thr Asn Gly Ala Gly Lys Asp Ala Leu Ala Gly Lys Pro
370 375 380

Leu Gln Ala Asp Ala Thr Leu Leu Val Asp Ala Thr Val Ala Ala Ala
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Ala Lys Asp Thr Ile Arg Lys Leu Tyr Asn Tyr Gln Gln Phe Ile Thr
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Gly Phe Ser Thr Val Gln Met Ile Asn Met Met Gly Ile Asn Ala Gly
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Trp His Asn Glu Glu Gly Tyr Ala Asp Asn Lys Thr Pro Asp Ala Gln
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530 535 540

Ala Ala Lys Ile Ala Asp Gln Val Tyr Val Thr Ser Pro Asp Asp Trp
545 550 555 560

Ala Thr Ser Ser Met Lys Lys Ala Gln Ala Ser Leu Glu Thr Asp Glu
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580 585 590

Asn Met Leu Tyr Ile Lys Glu Asp Thr Thr Ala Thr Pro Val Glu Pro
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Val Thr Asn Gln Ala Gly Lys Lys Val Asp Asn Thr Val Thr Ser Glu
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660 665 670

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Asp Ser Ile Thr Thr Pro Ala Ser Glu Ala Ala Ser Thr Ala Ala Ser
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Thr Val Ser Ser Glu Val Ser Glu Ser Val Thr Val Ser Ser Glu Pro
725 730 735

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740 745 750

Pro Thr Thr Thr Ala Ile Ser Glu Ser His Ala Val Val Glu Pro Val
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Ala Ser Leu Thr Glu Ser Glu Ser Gln Ala Ser Thr Ser Leu Val Ser
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<212> DNA
<213> *Trichoderma longibrachiatum*

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accagttcg agacgtcggg tgccatcaac cgatactatg tccagaatgg cgtcactttc    1260
cagcagccca acgccgagct tggtagttac tctggcaacg agctcaacga tgattactgc    1320
acagctgagg agacagaatt cggcggatct ctttctcaga caagggcggc ctgactcagt    1380
tcaagaaggc tacctctggc ggcattggtc tggatcatgag tctgtgggat gatgtgagtt    1440

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tgatggacaa acatgcgcgt tgacaaagag tcaagcagct gactgagatg ttacagtact 1500
acgccaacat gctgtggctg gactccacct acccgacaaa cgagacctcc tccacacccg 1560
gtgccgtgcg cggaagctgc tccaccagct ccggtgtccc tgctcaggtc gaatctcagt 1620
ctcccaacgc caaggtcacc ttctccaaca tcaagttcgg acccattggc agcacccggca 1680
accctagcgg cggaaccct cccggcgga accgtggcac caccaccacc cgccgcccag 1740
ccactaccac tggaagctct cccggaccta cccagtctca ctacggccag tgcggcggtg 1800
ttggctacag cgccccacg gtctgcgcca gcggcacaac ttgccaggtc ctgaaccctt 1860
actactctca gtgcctgtaa agctccgtgc gaaagcctga cgcaccggta gattcttggg 1920
gagcccgat catgacggcg gcgggagcta catggccccg ggtgatttat tttttttgta 1980
tctacttctg acccttttca aatatacgg caactcatct ttcactggag atgcggcctg 2040
cttgggtattg cgatgttgtc agcttgga attgtggctt tcgaaaacac aaaacgattc 2100
cttagtagcc atgcatttta agataacgga atagaagaaa gaggaatta aaaaaaaaaa 2160
aaaaacaaac atcccgttca taaccgtag aatcgccgct ctctgtgtat cccagtacca 2220

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<210> 11
<211> 1263
<212> DNA
<213> Phanerochaete chrysosporium

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<220>
<221> CDS
<222> (34)..(1152)
<223> ckg4 ligninase precursor

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<400> 11

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gctacagctc accgtccggt ctcagcagca gca atg gcg ttc aag cag ctc ctc 54
                               Met Ala Phe Lys Gln Leu Leu
                               1               5

gca gcc ctc tcc gtc gcc ctg acc ctc cag gtc acc caa gct gcc ccg 102
Ala Ala Leu Ser Val Ala Leu Thr Leu Gln Val Thr Gln Ala Ala Pro
      10               15               20

aac ctc gac aag cgc gtc gct tgc ccc gac ggc gtg cac acc gcc tcc 150
Asn Leu Asp Lys Arg Val Ala Cys Pro Asp Gly Val His Thr Ala Ser
      25               30               35

aac gcg gcg tgc tgt gca tgg ttc ccg gtc ctc gat gat atc cag cag 198
Asn Ala Ala Cys Cys Ala Trp Phe Pro Val Leu Asp Asp Ile Gln Gln
      40               45               50               55

aac ctc ttc cac ggt ggc cag tgc ggt gcc gag gcc cac gag gcc ctt 246
Asn Leu Phe His Gly Gly Gln Cys Gly Ala Glu Ala His Glu Ala Leu
      60               65               70

cgt atg gtc ttc cac gac tcc atc gct atc tcg ccc aag ctt cag tcg 294
Arg Met Val Phe His Asp Ser Ile Ala Ile Ser Pro Lys Leu Gln Ser
      75               80               85

cag ggc aag ttt ggc ggc ggc ggc gcg gac ggc tcg atc att acc ttc 342

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Gln	Gly	Lys	Phe	Gly	Gly	Gly	Gly	Ala	Asp	Gly	Ser	Ile	Ile	Thr	Phe	
90							95					100				
tcc	tcg	atc	gag	acc	acg	tac	cac	ccg	aac	atc	ggc	ctc	gac	gag	gtc	390
Ser	Ser	Ile	Glu	Thr	Thr	Tyr	His	Pro	Asn	Ile	Gly	Leu	Asp	Glu	Val	
105						110					115					
gtc	gcc	atc	cag	aag	ccg	ttc	atc	gcg	aag	cac	ggc	gtc	acc	cgt	ggc	438
Val	Ala	Ile	Gln	Lys	Pro	Phe	Ile	Ala	Lys	His	Gly	Val	Thr	Arg	Gly	
120					125					130					135	
gac	ttc	atc	gca	ttc	gct	ggc	gcc	gtc	ggc	gtg	agc	aac	tgc	ccg	ggc	486
Asp	Phe	Ile	Ala	Phe	Ala	Gly	Ala	Val	Gly	Val	Ser	Asn	Cys	Pro	Gly	
				140					145					150		
gcg	ccg	cag	atg	cag	ttc	ttc	ctt	ggc	cgc	ccc	gag	gca	acg	cag	gcc	534
Ala	Pro	Gln	Met	Gln	Phe	Phe	Leu	Gly	Arg	Pro	Glu	Ala	Thr	Gln	Ala	
			155					160					165			
gcc	ccc	gac	ggc	ctc	gtg	ccc	gag	ccc	ttc	cac	acc	atc	gat	cag	gtt	582
Ala	Pro	Asp	Gly	Leu	Val	Pro	Glu	Pro	Phe	His	Thr	Ile	Asp	Gln	Val	
		170					175					180				
ctc	gct	cgc	atg	ctt	gac	gct	ggc	ggc	ttc	gac	gag	atc	gag	act	gtc	630
Leu	Ala	Arg	Met	Leu	Asp	Ala	Gly	Gly	Phe	Asp	Glu	Ile	Glu	Thr	Val	
	185					190					195					
tgg	ctg	ctc	tct	gcc	cac	tcc	atc	gcg	gct	gcg	aac	gac	gtc	gac	ccg	678
Trp	Leu	Leu	Ser	Ala	His	Ser	Ile	Ala	Ala	Ala	Asn	Asp	Val	Asp	Pro	
200					205					210					215	
acc	atc	tcc	ggc	ctg	ccg	ttc	gac	tcc	act	ccc	ggc	cag	ttc	gac	tcc	726
Thr	Ile	Ser	Gly	Leu	Pro	Phe	Asp	Ser	Thr	Pro	Gly	Gln	Phe	Asp	Ser	
				220					225					230		
cag	ttc	ttc	gtc	gag	acg	cag	ctc	cgc	ggc	acc	gca	ttc	cct	ggc	aag	774
Gln	Phe	Phe	Val	Glu	Thr	Gln	Leu	Arg	Gly	Thr	Ala	Phe	Pro	Gly	Lys	
			235					240					245			
act	ggc	atc	cag	ggc	acc	gtc	atg	tcc	ccg	ctc	aag	ggc	gag	atg	cgt	822
Thr	Gly	Ile	Gln	Gly	Thr	Val	Met	Ser	Pro	Leu	Lys	Gly	Glu	Met	Arg	
		250					255					260				
ctg	cag	acg	gac	cac	ttg	ttc	gcg	cgt	gac	tcg	cgc	acg	gca	tgc	gag	870
Leu	Gln	Thr	Asp	His	Leu	Phe	Ala	Arg	Asp	Ser	Arg	Thr	Ala	Cys	Glu	
	265					270					275					
tgg	cag	tcc	ttc	gtc	aac	aac	cag	acg	aag	ctg	cag	gag	gac	ttc	cag	918
Trp	Gln	Ser	Phe	Val	Asn	Asn	Gln	Thr	Lys	Leu	Gln	Glu	Asp	Phe	Gln	
280					285					290					295	
ttc	atc	ttc	acg	gcg	ctc	tcg	acg	ctc	ggc	cac	gac	atg	aac	gcc	atg	966
Phe	Ile	Phe	Thr	Ala	Leu	Ser										

Cys Ala Ser Thr Pro Phe Pro Thr Leu Ile Thr Ala Pro Gly Pro Ser
 345 350 355
 gcg tcc gtc gct cgc atc ccc ccg ccg ccg tcc ccc aac taa 1152
 Ala Ser Val Ala Arg Ile Pro Pro Pro Pro Ser Pro Asn
 360 365 370
 gctatgtcta tgctggacat gctctcggtt ctacctcgtc ggtatcgctc cacggttatc 1212
 tcgcgttttgc atcatgtata cctgctcgtg gaatatacaa agtggtctat c 1263

<210> 12
 <211> 372
 <212> PRT
 <213> Phanerochaete chrysosporium

<400> 12

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Gln Val Thr Gln Ala Ala Pro Asn Leu Asp Lys Arg Val Ala Cys Pro
 20 25 30

Asp Gly Val His Thr Ala Ser Asn Ala Ala Cys Cys Ala Trp Phe Pro
 35 40 45

Val Leu Asp Asp Ile Gln Gln Asn Leu Phe His Gly Gly Gln Cys Gly
 50 55 60

Ala Glu Ala His Glu Ala Leu Arg Met Val Phe His Asp Ser Ile Ala
 65 70 75 80

Ile Ser Pro Lys Leu Gln Ser Gln Gly Lys Phe Gly Gly Gly Gly Ala
 85 90 95

Asp Gly Ser Ile Ile Thr Phe Ser Ser Ile Glu Thr Thr Tyr His Pro
 100 105 110

Asn Ile Gly Leu Asp Glu Val Val Ala Ile Gln Lys Pro Phe Ile Ala
 115 120 125

Lys His Gly Val Thr Arg Gly Asp Phe Ile Ala Phe Ala Gly Ala Val
 130 135 140

Gly Val Ser Asn Cys Pro Gly Ala Pro Gln Met Gln Phe Phe Leu Gly
 145 150 155 160

Arg Pro Glu Ala Thr Gln Ala Ala Pro Asp Gly Leu Val Pro Glu Pro
 165 170 175

Phe His Thr Ile Asp Gln Val Leu Ala Arg Met Leu Asp Ala Gly Gly

180

185

190

Phe Asp Glu Ile Glu Thr Val Trp Leu Leu Ser Ala His Ser Ile Ala
195 200 205

Ala Ala Asn Asp Val Asp Pro Thr Ile Ser Gly Leu Pro Phe Asp Ser
210 215 220

Thr Pro Gly Gln Phe Asp Ser Gln Phe Phe Val Glu Thr Gln Leu Arg
225 230 235 240

Gly Thr Ala Phe Pro Gly Lys Thr Gly Ile Gln Gly Thr Val Met Ser
245 250 255

Pro Leu Lys Gly Glu Met Arg Leu Gln Thr Asp His Leu Phe Ala Arg
260 265 270

Asp Ser Arg Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Thr
275 280 285

Lys Leu Gln Glu Asp Phe Gln Phe Ile Phe Thr Ala Leu Ser Thr Leu
290 295 300

Gly His Asp Met Asn Ala Met Ile Asp Cys Ser Glu Val Ile Pro Ala
305 310 315 320

Pro Lys Pro Val Asn Phe Gly Pro Ser Phe Phe Pro Ala Gly Lys Thr
325 330 335

His Ala Asp Ile Glu Gln Ala Cys Ala Ser Thr Pro Phe Pro Thr Leu
340 345 350

Ile Thr Ala Pro Gly Pro Ser Ala Ser Val Ala Arg Ile Pro Pro Pro
355 360 365

Pro Ser Pro Asn
370

<210> 13
<211> 1285
<212> DNA
<213> Phanerochaete chrysosporium

<220>
<221> CDS
<222> (34)..(1149) <223> CKG5 ligninase precursor
<400> 13

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Met Ala Phe Lys Lys Leu Leu

54

1

5

gct	ggt	ctt	acc	gcc	gct	ctc	tcc	ctc	cgc	gct	gcg	cag	ggt	gcg	gcc	102
Ala	Val	Leu	Thr	Ala	Ala	Leu	Ser	Leu	Arg	Ala	Ala	Gln	Gly	Ala	Ala	
		10					15					20				
gtc	gag	aag	cgc	gcg	acc	tgc	tcg	aac	ggc	aag	gtc	gtc	ccc	gcg	gcg	150
Val	Glu	Lys	Arg	Ala	Thr	Cys	Ser	Asn	Gly	Lys	Val	Val	Pro	Ala	Ala	
	25					30					35					
tct	tgc	tgc	acc	tgg	ttc	aac	ggt	ctg	tcc	gat	atc	cag	gag	aac	ctc	198
Ser	Cys	Cys	Thr	Trp	Phe	Asn	Val	Leu	Ser	Asp	Ile	Gln	Glu	Asn	Leu	
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ttc	aat	ggc	ggc	cag	tgt	ggc	gcc	gag	gct	cat	gag	tcg	atc	cgt	ctc	246
Phe	Asn	Gly	Gly	Gln	Cys	Gly	Ala	Glu	Ala	His	Glu	Ser	Ile	Arg	Leu	
				60					65					70		
gtc	ttc	cac	gac	gcc	atc	gct	atc	tct	ccc	gct	atg	gag	ccg	cag	gcc	294
Val	Phe	His	Asp	Ala	Ile	Ala	Ile	Ser	Pro	Ala	Met	Glu	Pro	Gln	Ala	
			75					80					85			
agt	tcg	gtg	cga	ggc	gcc	gat	ggg	tct	atc	atg	atc	ttc	gac	gag	atc	342
Ser	Ser	Val	Arg	Gly	Ala	Asp	Gly	Ser	Ile	Met	Ile	Phe	Asp	Glu	Ile	
		90					95					100				
gag	acc	aac	ttc	cat	ccc	aac	atc	ggg	ctc	gac	gag	atc	gtc	cgc	ctg	390
Glu	Thr	Asn	Phe	His	Pro	Asn	Ile	Gly	Leu	Asp	Glu	Ile	Val	Arg	Leu	
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cag	aag	ccg	ttc	gtc	cag	aag	cac	ggg	gtc	act	ccc	ggg	gac	ttc	atc	438
Gln	Lys	Pro	Phe	Val	Gln	Lys	His	Gly	Val	Thr	Pro	Gly	Asp	Phe	Ile	
120					125					130					135	
gcc	ttc	gct	ggc	gcg	gtg	gcg	ctc	agt	aac	tgc	ccc	ggg	gct	ccg	cag	486
Ala	Phe	Ala	Gly	Ala	Val	Ala	Leu	Ser	Asn	Cys	Pro	Gly	Ala	Pro	Gln	
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atg	aac	ttc	ttc	act	ggg	cgt	gct	ccg	gca	act	cag	cca	gcc	cct	gac	534
Met	Asn	Phe	Phe	Thr	Gly	Arg	Ala	Pro	Ala	Thr	Gln	Pro	Ala	Pro	Asp	
			155					160					165			
ggc	ctc	gtc	cca	gag	ccc	ttc	cac	tct	gtt	gac	caa	atc	atc	gac	cgt	582
Gly	Leu	Val	Pro	Glu	Pro	Phe	His	Ser	Val	Asp	Gln	Ile	Ile	Asp	Arg	
		170					175					180				
gtc	ttc	gat	gcc	ggg	gaa	ttc	gat	gag	ctc	gag	ctc	gtc	tgg	atg	ctc	630
Val	Phe	Asp	Ala	Gly	Glu	Phe	Asp	Glu	Leu	Glu	Leu	Val	Trp	Met	Leu	
	185					190					195					
tct	gca	cac	tcc	gtc	gcg	gct	gcc	aac	gat	atc	gac	ccg	aac	atc	cag	678
Ser	Ala	His	Ser	Val	Ala	Ala	Ala	Asn	Asp	Ile	Asp	Pro	Asn	Ile	Gln	
200					205					210					215	
ggc	ttg	ccc	ttc	gac	tcg	acc	ccc	ggg	att	ttc	gat	tcc	cag	ttc	ttc	726
Gly	Leu	Pro	Phe	Asp	Ser	Thr	Pro	Gly	Ile	Phe	Asp	Ser	Gln	Phe	Phe	
				220					225					230		
gtc	gag	act	cag	ctt	gct	ggc	acc	ggc	ttc	act	ggc	ggg	tct	aac	aac	774
Val	Glu	Thr	Gln	Leu	Ala	Gly	Thr	Gly	Phe	Thr	Gly	Gly	Ser	Asn	Asn	
			235					240					245			
cag	ggc	gag	gtt	tcc	tcc	ccg	ctt	cca	ggc	gag	atg	cgt	ctc	cag	tct	822
Gln	Gly	Glu	Val	Ser	Ser	Pro	Leu	Pro	Gly	Glu	Met	Arg	Leu	Gln	Ser	

gac ttc ctg atc gct cgt gac gcg cgc acc gcc tgc gag tgg cag tcg 870
 Asp Phe Leu Ile Ala Arg Asp Ala Arg Thr Ala Cys Glu Trp Gln Ser
 265 270 275

ttc gtc aac aac cag tcc aag ctc gtc tcc gac ttc caa ttc atc ttc 918
 Phe Val Asn Asn Gln Ser Lys Leu Val Ser Asp Phe Gln Phe Ile Phe
 280 285 290 295

ctc gcc ctc act cag ctc ggc cag gac ccg gat gcg atg acc gac tgc 966
 Leu Ala Leu Thr Gln Leu Gly Gln Asp Pro Asp Ala Met Thr Asp Cys
 300 305 310

tct gct gtc atc ccc atc tcc aag ccc gcc ccg aac aac acc ccc gga 1014
 Ser Ala Val Ile Pro Ile Ser Lys Pro Ala Pro Asn Asn Thr Pro Gly
 315 320 325

ttc tcc ttc ttc ccg ccc ggc atg acg atg gac gat gtc gag cag gct 1062
 Phe Ser Phe Phe Pro Pro Gly Met Thr Met Asp Asp Val Glu Gln Ala
 330 335 340

tgc gcc gag acg ccc ttc ccg act ctc tcg act ctc cct ggc ccc gcg 1110
 Cys Ala Glu Thr Pro Phe Pro Thr Leu Ser Thr Leu Pro Gly Pro Ala
 345 350 355

acc tcc gtc gct cgc atc cct cct cct cct ggt gct taa gcagccatca 1159
 Thr Ser Val Ala Arg Ile Pro Pro Pro Pro Gly Ala
 360 365 370

gacttcggat cacaccccggt tattggcaac ggaaatttag aacgaagatc gtccagtgtt 1219

ttgaagtaga aatgtgcttg tactgtgtaa acagctcttt tgacgaaata cactctgatt 1279

tcgtcg 1285

<210> 14
 <211> 371
 <212> PRT
 <213> Phanerochaete chrysosporium

<400> 14

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Arg Ala Ala Gln Gly Ala Ala Val Glu Lys Arg Ala Thr Cys Ser Asn
 20 25 30

Gly Lys Val Val Pro Ala Ala Ser Cys Cys Thr Trp Phe Asn Val Leu
 35 40 45

Ser Asp Ile Gln Glu Asn Leu Phe Asn Gly Gly Gln Cys Gly Ala Glu
 50 55 60

Ala His Glu Ser Ile Arg Leu Val Phe His Asp Ala Ile Ala Ile Ser
 65 70 75 80

Pro Ala Met Glu Pro Gln Ala Ser Ser Val Arg Gly Ala Asp Gly Ser
 85 90 95

Ile Met Ile Phe Asp Glu Ile Glu Thr Asn Phe His Pro Asn Ile Gly
 100 105 110

Leu Asp Glu Ile Val Arg Leu Gln Lys Pro Phe Val Gln Lys His Gly
 115 120 125

Val Thr Pro Gly Asp Phe Ile Ala Phe Ala Gly Ala Val Ala Leu Ser
 130 135 140

Asn Cys Pro Gly Ala Pro Gln Met Asn Phe Phe Thr Gly Arg Ala Pro
 145 150 155 160

Ala Thr Gln Pro Ala Pro Asp Gly Leu Val Pro Glu Pro Phe His Ser
 165 170 175

Val Asp Gln Ile Ile Asp Arg Val Phe Asp Ala Gly Glu Phe Asp Glu
 180 185 190

Leu Glu Leu Val Trp Met Leu Ser Ala His Ser Val Ala Ala Ala Asn
 195 200 205

Asp Ile Asp Pro Asn Ile Gln Gly Leu Pro Phe Asp Ser Thr Pro Gly
 210 215 220

Ile Phe Asp Ser Gln Phe Phe Val Glu Thr Gln Leu Ala Gly Thr Gly
 225 230 235 240

Phe Thr Gly Gly Ser Asn Asn Gln Gly Glu Val Ser Ser Pro Leu Pro
 245 250 255

Gly Glu Met Arg Leu Gln Ser Asp Phe Leu Ile Ala Arg Asp Ala Arg
 260 265 270

Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Ser Lys Leu Val
 275 280 285

Ser Asp Phe Gln Phe Ile Phe Leu Ala Leu Thr Gln Leu Gly Gln Asp
 290 295 300

Pro Asp Ala Met Thr Asp Cys Ser Ala Val Ile Pro Ile Ser Lys Pro
 305 310 315 320

Ala Pro Asn Asn Thr Pro Gly Phe Ser Phe Phe Pro Pro Gly Met Thr
 325 330 335

Met Asp Asp Val Glu Gln Ala Cys Ala Glu Thr Pro Phe Pro Thr Leu
 340 345 350

Ser Thr Leu Pro Gly Pro Ala Thr Ser Val Ala Arg Ile Pro Pro Pro
 355 360 365

Pro Gly Ala
 370

<210> 15
 <211> 360
 <212> DNA
 <213> Solanum tuberosum

<400> 15

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 taataactaa ttatctgaat aagagaaaga gagatcatcc atatttctta tcctaaatga 180
 atgacagtgt ctttataatt ctttgatgaa cagatgcatt ttattaacca attccatata 240
 catataaata ttaatcatat ataattaata tcaattgggt agcaaaaacc aaatctagtc 300
 taggtgtgtt ttgctaatta tgggggatag agcaaaaaag aaactaacgt ctcaagaatc 360

<210> 16
 <211> 2521
 <212> DNA
 <213> Agrobacterium tumefaciens

<220>
 <221> CDS
 <222> (585)..(1826)
 <223> nopaline synthetase

<400> 16

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 aaccctgtgg ttggcatgca catacaaatg gacgaacgga taaacctttt cagccctttt 180
 taaatatccg ttattctaata aaacgctctt ttctcttagg tttaccgccc aatataatcct 240
 gtcaaact gatagtttaa actgaaggcg ggaaacgaca atctgatcat gagcggagaa 300
 ttaaggaggt cacgttatga cccccgccga tgacgcggga caagccgttt tacgtttgga 360
 actgacagaa ccgcaacgat tgaaggagcc actcagccgc gggtttctgg agtttaatga 420
 gctaagcaca tacgtcagaa accattattg cgcgttcaaa agtcgcctaa ggtcactatc 480
 agctagcaaa tatttcttgt caaaaatgct cactgacgt tccataaatt cccctcggtg 540
 tccaattaga gtctcatatt cactctcaat ccaaataatc tgca atg gca att acc 596
 Met Ala Ile Thr

tta tcc gca act tct tta cct att tcc gcc gca gat cac cat ccg ctt	644
Leu Ser Ala Thr Ser Leu Pro Ile Ser Ala Ala Asp His His Pro Leu	
5 10 15 20	
ccc ttg acc gta ggt gtc ctc ggt tct ggt cac gcg ggg act gca tta	692
Pro Leu Thr Val Gly Val Leu Gly Ser Gly His Ala Gly Thr Ala Leu	
25 30 35	
gcg gct tgg ttc gcc tcc cgg cat gtt ccc acg gcg ctg tgg gca cca	740
Ala Ala Trp Phe Ala Ser Arg His Val Pro Thr Ala Leu Trp Ala Pro	
40 45 50	
gca gat cat cca gga tcg atc tca gca atc aag gcc aat gaa gga gtt	788
Ala Asp His Pro Gly Ser Ile Ser Ala Ile Lys Ala Asn Glu Gly Val	
55 60 65	
atc acc acc gag gga atg att aac ggt cca ttt agg gtc tca gcc tgt	836
Ile Thr Thr Glu Gly Met Ile Asn Gly Pro Phe Arg Val Ser Ala Cys	
70 75 80	
gat gac ctt gcc gca gtt att cgc tcc agc cgt gta ctg att att gta	884
Asp Asp Leu Ala Ala Val Ile Arg Ser Ser Arg Val Leu Ile Ile Val	
85 90 95 100	
acc cgt gcg gac gtt cac gac agc ttc gtc aac gaa ctc gcc aac ttc	932
Thr Arg Ala Asp Val His Asp Ser Phe Val Asn Glu Leu Ala Asn Phe	
105 110 115	
aac ggc gaa ctc gca aca aag gat att gtc gtc gtg tgc ggc cat ggc	980
Asn Gly Glu Leu Ala Thr Lys Asp Ile Val Val Val Cys Gly His Gly	
120 125 130	
ttc tcc atc aag tac gag aga cag ctg cga ttc aag cga ata ttc gag	1028
Phe Ser Ile Lys Tyr Glu Arg Gln Leu Arg Phe Lys Arg Ile Phe Glu	
135 140 145	
acg gat aat tcg ccc ata acg tct aag cta tcg gat caa aaa aaa tgt	1076
Thr Asp Asn Ser Pro Ile Thr Ser Lys Leu Ser Asp Gln Lys Lys Cys	
150 155 160	
aac gtc aac atc aag gaa atg aaa gcg tct ttc gga ctg tca tgt ttc	1124
Asn Val Asn Ile Lys Glu Met Lys Ala Ser Phe Gly Leu Ser Cys Phe	
165 170 175 180	
cca att cat cgc gat gat gct ggc gtg att gat cta ccc gaa gat acc	1172
Pro Ile His Arg Asp Asp Ala Gly Val Ile Asp Leu Pro Glu Asp Thr	
185 190 195	
aag aac atc ttt gcc cag cta ttt tcc gct aga atc atc tgc atc ccg	1220
Lys Asn Ile Phe Ala Gln Leu Phe Ser Ala Arg Ile Ile Cys Ile Pro	
200 205 210	
ccg ttg caa gtg cta ttc ttt tcc aac tgt atc act cat gcg gtt ccg	1268
Pro Leu Gln Val Leu Phe Phe Ser Asn Cys Ile Thr His Ala Val Pro	
215 220 225	
gca gtc atg aac atc gga aga ctc cgc gac cca gcc aat tct ctt act	1316
Ala Val Met Asn Ile Gly Arg Leu Arg Asp Pro Ala Asn Ser Leu Thr	
230 235 240	
aaa aga gct gag aag tgg ctt ctt gaa cta gac gag cga acc cca cga	1364
Lys Arg Ala Glu Lys Trp Leu Leu Glu Leu Asp Glu Arg Thr Pro Arg	

245	250	255	260	
gcc gag aag ggc ttt ttc ttt tat ggt gaa gga tcc aac act tac gtt Ala Glu Lys Gly Phe Phe Phe Tyr Gly Glu Gly Ser Asn Thr Tyr Val 265 270 275				1412
tgc aac gtc caa gag caa ata gac cac gaa cgc cgg aag gtt gcc gca Cys Asn Val Gln Glu Gln Ile Asp His Glu Arg Arg Lys Val Ala Ala 280 285 290				1460
gcg tgt gga ttg cgt ctc aat tct ctc ttg cag gaa tgc aat gat gaa Ala Cys Gly Leu Arg Leu Asn Ser Leu Leu Gln Glu Cys Asn Asp Glu 295 300 305				1508
tat gat act gac tat gaa act ttg agg gaa tac tgc cta gca ccg tca Tyr Asp Thr Asp Tyr Glu Thr Leu Arg Glu Tyr Cys Leu Ala Pro Ser 310 315 320				1556
cct cat aac gtg cat cat gca tgc cct gac aac atg gaa cat cgc tat Pro His Asn Val His His Ala Cys Pro Asp Asn Met Glu His Arg Tyr 325 330 335 340				1604
ttt tct gaa gaa tta tgc tcg ttg gag gat gtc gcg gca att gca gct Phe Ser Glu Glu Leu Cys Ser Leu Glu Asp Val Ala Ala Ile Ala Ala 345 350 355				1652
att gcc aac atc gaa cta ccc ctc acg cat gca ttc atc aat att att Ile Ala Asn Ile Glu Leu Pro Leu Thr His Ala Phe Ile Asn Ile Ile 360 365 370				1700
cat gcg ggg aaa ggc aag att aat cca act ggc aaa tca tcc agc gtg His Ala Gly Lys Gly Lys Ile Asn Pro Thr Gly Lys Ser Ser Ser Val 375 380 385				1748
att ggt aac ttc agt tcc agc gac ttg att cgt ttt ggt gct acc cac Ile Gly Asn Phe Ser Ser Ser Asp Leu Ile Arg Phe Gly Ala Thr His 390 395 400				1796
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Gly Thr Ala Leu Ala Ala Trp Phe Ala Ser Arg His Val Pro Thr Ala
35 40 45

Leu Trp Ala Pro Ala Asp His Pro Gly Ser Ile Ser Ala Ile Lys Ala
50 55 60

Asn Glu Gly Val Ile Thr Thr Glu Gly Met Ile Asn Gly Pro Phe Arg
65 70 75 80

Val Ser Ala Cys Asp Asp Leu Ala Ala Val Ile Arg Ser Ser Arg Val
85 90 95

Leu Ile Ile Val Thr Arg Ala Asp Val His Asp Ser Phe Val Asn Glu
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Leu Ala Asn Phe Asn Gly Glu Leu Ala Thr Lys Asp Ile Val Val Val
115 120 125

Cys Gly His Gly Phe Ser Ile Lys Tyr Glu Arg Gln Leu Arg Phe Lys
130 135 140

Arg Ile Phe Glu Thr Asp Asn Ser Pro Ile Thr Ser Lys Leu Ser Asp
145 150 155 160

Gln Lys Lys Cys Asn Val Asn Ile Lys Glu Met Lys Ala Ser Phe Gly
165 170 175

Leu Ser Cys Phe Pro Ile His Arg Asp Asp Ala Gly Val Ile Asp Leu
180 185 190

Pro Glu Asp Thr Lys Asn Ile Phe Ala Gln Leu Phe Ser Ala Arg Ile
195 200 205

Ile Cys Ile Pro Pro Leu Gln Val Leu Phe Phe Ser Asn Cys Ile Thr
210 215 220

His Ala Val Pro Ala Val Met Asn Ile Gly Arg Leu Arg Asp Pro Ala
225 230 235 240

Asn Ser Leu Thr Lys Arg Ala Glu Lys Trp Leu Leu Glu Leu Asp Glu
245 250 255

Arg Thr Pro Arg Ala Glu Lys Gly Phe Phe Phe Tyr Gly Glu Gly Ser
260 265 270

Asn Thr Tyr Val Cys Asn Val Gln Glu Gln Ile Asp His Glu Arg Arg
275 280 285

Lys Val Ala Ala Ala Cys Gly Leu Arg Leu Asn Ser Leu Leu Gln Glu
290 295 300

Cys Asn Asp Glu Tyr Asp Thr Asp Tyr Glu Thr Leu Arg Glu Tyr Cys
305 310 315 320

Leu Ala Pro Ser Pro His Asn Val His His Ala Cys Pro Asp Asn Met
325 330 335

Glu His Arg Tyr Phe Ser Glu Glu Leu Cys Ser Leu Glu Asp Val Ala
340 345 350

Ala Ile Ala Ala Ile Ala Asn Ile Glu Leu Pro Leu Thr His Ala Phe
355 360 365

Ile Asn Ile Ile His Ala Gly Lys Gly Lys Ile Asn Pro Thr Gly Lys
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<211> 835

<212> DNA

<213> Streptomyces hygrosopicus

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ccggttccgg caccgaggaa gaccgaagga agaccacacg tgagcccaga acgacgcccg 180

gccgacatcc gccgtgccac cgaggcggac atgccggcgg tctgcaccat cgtcaaccac 240

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25

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